CLAIMS

1. A method for detecting the genotype in a nucleic acid sample, the method comprising the following step (a):

(a) analyzing two or more polymorphisms selected from the group consisting of the following (1) to (4) in a nucleic acid sample:

(1) a polymorphism at the base number position 1648 of the glycoprotein Ia gene;

(2) a polymorphism at the base number position 190 of the chemokine receptor 2 gene;

(3) a polymorphism at the base number position 1100 of the apolipoprotein C-III gene; and

(4) a polymorphism at the base number position 825 of G-protein β3 subunit gene.

2. A method for detecting the genotype in a nucleic acid sample, the method comprising the following step (b):

(b) analyzing two or more polymorphisms selected from the group consisting of the following (5) to (8) in a nucleic acid sample:

(5) a polymorphism at the base number position -850 of the tumor necrosis factor-α gene;

(6) a polymorphism at the base number position -238 of the tumor necrosis factor-α gene;

(7) a polymorphism at the base number position 3494 of the insulin receptor substrate-1 gene; and

(8) a polymorphism at the base number position 1018 of the glycoprotein Ibα gene.

3. A method for diagnosing the risk for hypertension, the method comprising the following steps (i) to (iii):

(i) analyzing two or more polymorphisms selected from the group consisting of the following (1) to (4) in a nucleic acid sample:

(1) a polymorphism at the base number position 1648 of the glycoprotein Ia gene;

(2) a polymorphism at the base number position 190 of the chemokine receptor 2 gene;

(3) a polymorphism at the base number position 1100 of the apolipoprotein C-III gene; and

(4) a polymorphism at the base number position 825 of G-protein β3 subunit gene.

(ii) determining, based on the information about polymorphism which was obtained in the step (i), the genotype in the nucleic acid sample; and

(iii) assessing, based on the genotype determined, a genetic risk for hypertension.

4. A method for diagnosing the risk for hypertension, the method comprising the following steps (iv) to (vi):

(iv) analyzing two or more polymorphisms selected from the group consisting of the following (5) to (8) in a nucleic acid sample:

(5) a polymorphism at the base number position -850 of the tumor necrosis factor-α gene;

(6) a polymorphism at the base number position -238 of the tumor necrosis factor-α gene;

(7) a polymorphism at the base number position 3494 of the insulin receptor substrate-1 gene; and

(8) a polymorphism at the base number position 1018 of the glycoprotein Ibα gene.

(v) determining, based on the information about polymorphism which was obtained in the step (iv), the genotype in the nucleic acid sample; and

(vi) assessing, based on the genotype determined, a genetic risk for hypertension.

5. A kit for detecting the genotype, comprising two or more of nucleic acids selected from the group consisting of the following (1) to (4):

(1) a nucleic acid for analyzing a polymorphism at the base number position 1648 of the glycoprotein Ia gene;

(2) a nucleic acid for analyzing a polymorphism at the base number position 190 of the chemokine receptor 2 gene;

(3) a nucleic acid for analyzing a polymorphism at the base number position 1100 of the apolipoprotein C-III gene; and

(4) a nucleic acid for analyzing a polymorphism at the base number position 825 of G-protein β3 subunit gene.

6. A kit for detecting the genotype, comprising two or more of nucleic acids selected from the group consisting of the following (5) to (8):

(5) a nucleic acid for analyzing a polymorphism at the base number position -850 of the tumor necrosis factor-α gene;

(6) a nucleic acid for analyzing a polymorphism at the base number position -238 of the tumor necrosis factor-α gene;

(7) a nucleic acid for analyzing a polymorphism at the base number position

3494 of the insulin receptor substrate-1 gene; and

(8) a nucleic acid for analyzing a polymorphism at the base number position 1018 of the glycoprotein Ibα gene.

7. Fixed nucleic acids comprising the following two or more nucleic acids selected from the group consisting of the following (1) to (4) fixed to an insoluble support:

(1) a nucleic acid for analyzing a polymorphism at the base number position 1648 of the glycoprotein Ia gene;

(2) a nucleic acid for analyzing a polymorphism at the base number position 190 of the chemokine receptor 2 gene;

(3) a nucleic acid for analyzing a polymorphism at the base number position 1100 of the apolipoprotein C-III gene; and

(4) a nucleic acid for analyzing a polymorphism at the base number position 825 of G-protein β3 subunit gene.

8. Fixed nucleic acids comprising the following two or more nucleic acids selected from the group consisting of the following (5) to (8) fixed to an insoluble support:

(5) a nucleic acid for analyzing a polymorphism at the base number position -850 of the tumor necrosis factor-α gene;

(6) a nucleic acid for analyzing a polymorphism at the base number position -238 of the tumor necrosis factor-α gene;

(7) a nucleic acid for analyzing a polymorphism at the base number position 3494 of the insulin receptor substrate-1 gene; and

(8) a nucleic acid for analyzing a polymorphism at the base number position 1018 of the glycoprotein Ibα gene.